

10/607, 829

FILE 'HOME' ENTERED AT 14:26:13 ON 03 JUN 2004

=> file biosis medline caplus wpids uspatfull
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FILE 'CAPLUS' ENTERED AT 14:26:31 ON 03 JUN 2004
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FILE 'USPATFULL' ENTERED AT 14:26:31 ON 03 JUN 2004
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*** YOU HAVE NEW MAIL ***

=> s detect? (3a) polymorphism>
MISSING TERM AFTER LYMPHISM>
Operators must be followed by a search term, L-number, or query name.

=> s detect? (3a) polymorphism?
4 FILES SEARCHED...
L1 18021 DETECT? (3A) POLYMORPHISM?

=> s l1 and set (3a) probe?
L2 550 L1 AND SET (3A) PROBE?

=> s l2 and first (4a) probe?
L3 295 L2 AND FIRST (4A) PROBE?

=> s l3 and second (4a) probe?
L4 263 L3 AND SECOND (4A) PROBE?

=> s l4 and third (4a) probe?
L5 120 L4 AND THIRD (4A) PROBE?

=> s l5 and hybridization
L6 118 L5 AND HYBRIDIZATION

=> dup rem l6
PROCESSING COMPLETED FOR L6
L7 117 DUP REM L6 (1 DUPLICATE REMOVED)

=> s l7 and py<=1995
2 FILES SEARCHED...
4 FILES SEARCHED...
L8 0 L7 AND PY<=1995

=> s l7 known mismatch?
MISSING OPERATOR L7 KNOWN
The search profile that was entered contains terms or
nested terms that are not separated by a logical operator.

=> s l7 and known mismatch?

L9 2 L7 AND KNOWN MISMATCH?

=> d 19 bib abs 1-2

L9 ANSWER 1 OF 2 USPATFULL on STN
AN 2002:185584 USPATFULL
TI **Polymorphism detection**
IN Lipshutz, Robert J., Palo Alto, CA, UNITED STATES
Sapolsky, Ronald, Mountain View, CA, UNITED STATES
Ghandour, Ghassan, Atherton, CA, UNITED STATES
PI US 2002098496 A1 20020725
US 6586186 B2 20030701
AI US 2001-939119 A1 20010824 (9)
RLI Continuation of Ser. No. US 1997-853370, filed on 8 May 1997, GRANTED,
Pat. No. US 6300063 Continuation-in-part of Ser. No. US 1995-563762,
filed on 29 Nov 1995, GRANTED, Pat. No. US 5858659
PRAI US 1996-17260P 19960510 (60)
DT Utility
FS APPLICATION
LREP RITTER, LANG & KAPLAN, 12930 SARATOGA AE. SUITE D1, SARATOGA, CA, 95070
CLMN Number of Claims: 17
ECL Exemplary Claim: 1
DRWN 10 Drawing Page(s)
LN.CNT 885

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present invention generally provides a rapid efficient method for analyzing polymorphic or biallelic markers, and arrays for carrying out these analyses. In general, the methods of the present invention employ arrays of oligonucleotide probes that are complementary to target nucleic acids which correspond to the marker sequences of an individual. The probes are typically arranged in detection blocks, each block being capable of discriminating the three genotypes for a given marker, e.g., the heterozygote or either of the two homozygotes. The method allows for rapid, automatable analysis of genetic linkage to even complex polygenic traits.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L9 ANSWER 2 OF 2 USPATFULL on STN
AN 2001:173324 USPATFULL
TI **Polymorphism detection**
IN Lipshutz, Robert J., Palo Alto, CA, United States
Sapolsky, Ronald, Mountain View, CA, United States
Ghandour, Ghassan, Atherton, CA, United States
PA Affymetrix, Inc., Santa Clara, CA, United States (U.S. corporation)
PI US 6300063 B1 20011009
AI US 1997-853370 19970508 (8)
RLI Continuation-in-part of Ser. No. US 1995-563762, filed on 29 Nov 1995
PRAI US 1996-17260P 19960510 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Riley, Jezia
LREP Ritter, Lang & Kaplan LLP
CLMN Number of Claims: 20
ECL Exemplary Claim: 1
DRWN 14 Drawing Figure(s); 10 Drawing Page(s)
LN.CNT 1044

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present invention generally provides a rapid efficient method for analyzing polymorphic or biallelic markers, and arrays for carrying out these analyses. In general, the methods of the present invention employ arrays of oligonucleotide probes that are complementary to target nucleic acids which correspond to the marker sequences of an individual. The probes are typically arranged in detection blocks, each block being

capable of discriminating the three genotypes for a given marker, e.g., the heterozygote or either of the two homozygotes. The method allows for rapid, automatable analysis of genetic linkage to even complex polygenic traits.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

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=> d his

(FILE 'HOME' ENTERED AT 14:26:13 ON 03 JUN 2004)

FILE 'BIOSIS, MEDLINE, CAPLUS, WPIDS, USPATFULL' ENTERED AT 14:26:31 ON
03 JUN 2004

L1 18021 S DETECT? (3A) POLYMORPHISM?
L2 550 S L1 AND SET (3A) PROBE?
L3 295 S L2 AND FIRST (4A) PROBE?
L4 263 S L3 AND SECOND (4A) PROBE?
L5 120 S L4 AND THIRD (4A) PROBE?
L6 118 S L5 AND HYBRIDIZATION
L7 117 DUP REM L6 (1 DUPLICATE REMOVED)
L8 0 S L7 AND PY<=1995
L9 2 S L7 AND KNOWN MISMATCH?

=> s l7 and array?

L10 101 L7 AND ARRAY?

=> s l0 and py<=1998

2 FILES SEARCHED...

4 FILES SEARCHED...

L11 5719 L0 AND PY<=1998

=> s l10 and py<=1998

2 FILES SEARCHED...

4 FILES SEARCHED...

L12 2 L10 AND PY<=1998

=> d l12 bib abs 1-2

L12 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2004 ACS on STN

AN 2002:808367 CAPLUS

DN 137:321238

TI **Detection of genetic polymorphisms and gene copy
number using arrays**

IN Cronin, Maureen T.; Sheldon, Edward L.; Miyada, Charles G.; Hubbell, Earl
A.; Chee, Mark; Fodor, Stephen P. A.; Huang, Xiaohua C.; Lipshutz, Robert
J.; Lobban, Peter E.; Morris, MacDonald S.

PA Affymetrix, Inc., USA

SO U.S., 51 pp., Cont.-in-part of U.S. 6,309,823.

CODEN: USXXAM

DT Patent

LA English

FAN.CNT 16

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 6468744	B1	20021022	US 1999-341399	19991117
	US 6309823	B1	20011030	US 1997-778794	19970103
	WO 9830883	A2	19980716	WO 1998-US6414	19980102 <--
	WO 9830883	A3	19981029		

W: JP, US

RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE

PRAI US 1997-778794 A2 19970103
WO 1998-US6414 W 19980102
US 1993-143312 B2 19931026
US 1994-284064 B2 19940802
WO 1994-US12305 A2 19941026
US 1995-510521 A2 19950802
US 1995-544381 A2 19951010

AB The invention provides methods for detecting variations in polymorphic
sites and/or variations in gene copy number in an individual. The methods
are particularly useful for anal. of biotransformation genes, such as

cytochromes P 450. The invention provides **arrays** of immobilized probes, and methods employing the **arrays**, for detecting mutations in the biotransformation genes, such as cytochromes P 450. For example, one such **array** comprises four probe sets. A **first probe set** comprises a plurality of probes spanning a polymorphic site, each probe comprising a segment of at least six nucleotides exactly complementary to a subsequence of a polymorphic form at the site from a biotransformation gene, the segment including at least one interrogation position complementary to a corresponding nucleotide in the polymorphic form. **Second**, **third** and fourth **probe** sets each comprise a corresponding probe for each **probe** in the **first probe set**. The **probes** in the **second**, **third** and fourth **probe** sets are identical to a sequence comprising the corresponding **probe** from the **first probe set** or a subsequence of at least six nucleotides thereof that includes at least one interrogation position, except that the at least one interrogation position is occupied by a different nucleotide in each of the four corresponding probes from the four probe sets.

RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 2 OF 2 USPATFULL on STN
AN 2002:75200 USPATFULL
TI Method to **detect** gene **polymorphisms** and monitor
allelic expression employing a probe **array**
IN Chee, Mark, Del Mar, CA, United States
PA Affymetrix, Inc., Santa Clara, CA, United States (U.S. corporation)
PI US 6368799 B1 20020409
WO 9856954 19981217
AI US 2000-445734 20000314 (9)
WO 1998-US12442 19980611
20000314 PCT 371 date
PRAI US 1997-49612P 19970613 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Siew, Jeffrey
LREP Townsend and Townsend and Crew LLP
CLMN Number of Claims: 11
ECL Exemplary Claim: 1
DRWN 0 Drawing Figure(s); 0 Drawing Page(s)
LN.CNT 669

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The invention provides methods of monitoring expression levels of different polymorphic forms of a gene. Such methods entail analyzing genomic DNA from an individual to determine the presence of heterozygous polymorphic forms at a polymorphic site within a transcribed sequence of a gene of interest. RNA from a tissue of the individual in which the gene is expressed is then analyzed to determine relative proportions of polymorphic forms in transcript of the gene. Having identified alleles of a gene that are expressed at different levels, the alleles can be further analyzed to locate a second polymorphism that has a causative role in the different expression levels. The methods are amenable to analyzing large collections of genes simultaneously using **arrays** of immobilized probes.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

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